

Figure 1

	1				50
1	MSDRQAALDM	ALKQIEKQFG	KGSIMKLGEQ	UEURISUVPS	GSLALDAALG
2	MSDRQAALDM	ALKQIEKQFG	KGSIMKLGEK	TDTRISTVPS	GSLALDTALG
3	MSDRQAALDM	ALKQIEKQFG	KGSIMKLGEK	TDTRISTVPS	GSLALDTALG
4	MSDRQAALDM	ALKQIEKQFG	KGSIMKLGEK	TDTRISTVPS	GSLALDTALG
	51				100
1	VGGYPRGRII	EVYGPSSGK	UUVALHAI AE	VQQQGGQAAF	IDADUALDPV
2	IGGYPRGRII	EVYGPSSGK	TTVALHAI AE	VQEKGGQAAF	IDA EHALDPV
3	IGGYPRGRII	EVYGPSSGK	TTVALHAI AE	VQQQR.TSAF	IDA EHALDPV
4	IGGYPRGRII	EVYGPSSGK	TTVALHAI AE	VQQQR.TSAF	IDA EHALDPV
	101				150
1	YAQKLGVNID	ELLLSQPDUG	EQALEIAEAL	VRSGAVDIVV	IDSVAALVPK
2	YAQKLGVNIE	ELLLSQPDTG	EQALEIAEAL	VRSGAVDIVV	VDSVAALVPK
3	YAQKLGVNIE	ELLLSQPDTG	EQALEIAEAL	VRSGAVDIVV	VDSVAALVPK
4	YAQKLGVNIE	ELLLSQPDTG	EQALEIAEAL	VRSGAVDIVV	VDSVAALVPK
	151				200
1	AEIEGDMGDS	HVGLQARLMS	QALRKLSGAI	NKSKUIAIFI	NQIREKVGVM
2	AEIEGDMGDS	HVGLQARLMS	QALRKLSGAI	NKSKTIAIFI	NQIREKVGVM
3	AEIEGDMGDS	HVGLQARLMS	QALRKLSGAI	NKSKTIAIFI	NQIREKVGVM
4	AEIEGDMGDS	HVGLQARLMS	QALRKLSGAI	NKSKTIAIFI	NQIREKVGVM
	201				250
1	FGNPEUUPGG	RALKFYSSVR	LEVRRAEQLK	QGNDVMGNKU	KIKVVKNKVA
2	FGNPETTPGG	RALKFYSSVR	LEVRRAEQLK	QGNDVMGNKT	RIKVVKNKVA
3	FGNPETTPGG	RALKFYSSVR	LEVRRAEQLK	QGNDVMGNKT	KIKVVKNKVA
4	FGNPETTPGG	RALKFYSSVR	LEVRRAEQLK	QGNDVMGNKT	KIKVVKNKVA
	251				300
1	PPFRUA EVDI	MYGEGISKEG	EIIDLGUELD	IVQKSGAWYS	YQEEERLGQGR
2	PPFRTAEVDI	MYGEGISKEG	EIIDLGTELD	IVQKSGSWYS	YEEERLGQGR
3	PPFRTAEVDI	MYGEGISKEG	EIIDLGTELD	IVQKSGSWYS	YEEERLGQGR
4	PPFRTAEVDI	MYGEGISKEG	EIIDLGTELD	IVQKSGSWYS	YEEERLGQGR
	301				350
1	ENAKQFLKEN	KDILLMIQEQ	IREHYGLDUG	GAAPAQEDEA	QAQEELEF.S
2	ENAKQFLKEN	KDIMLMIQEQ	IREHYGLDNN	G...VTEKAE	EVQEELEFEE
3	ENAKQFLKEN	KDIMLMIQEQ	IREHYGLDNN	G...VVQQQAE	ETQEELEFEE
4	ENAKQFLKEN	KDIMLMIQEQ	IREHYGLDNN	G...VVQQQAE	ETQEELEFEE

Figure 2 / Part I

	1				50
1	ATGAGTGATC	GTCAGGCAGC	CTTAGATATG	GCGCTTAAAC	AAATAGAAAA
2	ATGAGTGATC	GTCAGGCAGC	CTTAGATATG	GCTCTTAAAGC	AAATAGAAAA
3	ATGAGTGATC	GTCAGGCAGC	CTTAGATATG	GCTCTTAAAC	AAATAGAAAA
4	ATGAGTGATC	GTCAGGCAGC	CTTAGATATG	GCTCTTAAAC	AAATAGAAAA
	51				100
1	GCAGTTTGGT	AAAGGTTCCA	TTATGAAACT	CGGCGAACAA	ACTGAAACGA
2	ACAATTTCGGC	AAAGGTTCCA	TCATGAAGCT	CGGAGAAAAA	ACGGATACAA
3	ACAGTTTCGGC	AAAGGTTCCA	TTATGAAACT	GGGAGAAAAG	ACAGATACAA
4	ACAGTTTCGGC	AAAGGTTCCA	TTATGAAACT	GGGAGAAAAG	ACAGATACAA
	101				150
1	GAATTTCAAC	AGTTCCGAGC	GGTTCTTTAG	CGCTCGATGC	GGCTCTTGGA
2	GAATTTCAAC	GGTGCCGAGC	GGTTCCCTTG	CACTTGATAC	CGCTCTCGGA
3	GAATTTCTAC	TGTACCAAGC	GGCTCCCTCG	CTCTTGATAC	AGCACTGCGA
4	GAATTTCTAC	TGTACCAAGC	GGCTCCCTCG	CTCTTGATAC	AGCACTGCGA
	151				200
1	GTGGGCGGAT	ACCCGCGCGG	CCGGATTATT	GAAGTATACG	GGCCTGAAAG
2	ATAGGCGGAT	ACCCGCGCGG	ACGGATTATT	GAAGTATACG	GACCTGAAAG
3	ATTGGGCGGAT	ATCCTCGCGG	ACGGATTATT	GAAGTATACG	GTCCTGAAAG
4	ATTGGGCGGAT	ATCCTCGCGG	ACGGATTATT	GAAGTATACG	GTCCTGAAAG
	201				250
1	CTCCGGTAAA	ACGACGGTGG	CGCTTCATGC	GATTGCCGAA	G TTCAGCAGC
2	CTCAGGTAAA	ACGACTGTAG	CGCTTCACGC	AATCGCTGAG	G TTCAGGAAA
3	CTCAGGTAAA	ACAACTGTGG	CGCTTCATGC	GATTGCTGAA	G TTCAGCAGC
4	CTCAGGTAAA	ACAACTGTGG	CGCTTCATGC	GATTGCTGAA	G TTCAGCAGC
	251				300
1	AGGGCGGACA	AGCGGCGTTC	ATCGACGCCG	ACACCGCGCT	TGATCCCGTC
2	AAGGCGGACA	GGCAGCATTT	ATTGATGCCG	AGCATGCTCT	TGATCCTGTG
3	A..GCGGACA	AGC.GCGTTT	ATCGATGCCG	AGCATGCGTT	AGATCCGGTA
4	A..GCGGACA	AGC.GCGTTT	ATCGATGCCG	AGCATGCGTT	AGATCCGGTA
	301				350
1	TATGCACAAA	AGCTGGGCGT	CAACATTGAT	GAGCTTTTGC	TGTCACAGCC
2	TACGCGCAAA	AGCTCGGTGT	CAATATCGAA	GAGCTGCTGC	TTTCTCAGCC
3	TACGCGCAAA	AGCTCGGTGT	TAACATCGAA	GAGCTTTTAC	TGTCTCAGCC
4	TACGCGCAAA	AGCTCGGTGT	TAACATCGAA	GAGCTTTTAC	TGTCTCAGCC

Figure 2 / Part II

	351				400
1	TGATACGGGC	GAGCAGGCGC	TCGAAATCGC	TGAAGCCCTT	GTCAGAAGCG
2	GGATACGGGA	GAGCAGGCGC	TGGAGATTGC	TGAAGCGCTG	GTGCGAAGCG
3	TGACACAGGC	GAGCAGGCGC	TTGAAATTGC	GGAAGCATTG	GTTCGAAGCG
4	TGACACAGGC	GAGCAGGCGC	TTGAAATTGC	GGAAGCATTG	GTTCGAAGCG
	401				450
1	GAGCGGTGGA	TATCGTTGTC	ATCGACTCTG	TAGCAGCGCT	TGTGCCGAAA
2	GAGCTGTCGA	TATCGTAGTC	GTTGACTCTG	TTGCGGCGCT	TGTTCCAAAA
3	GGGCAGTTGA	CATTGTCGTT	GTCGACTCTG	TAGCCGCTCT	CGTTCCGAAA
4	GGGCAGTTGA	CATTGTCGTT	GTCGACTCTG	TAGCCGCTCT	CGTTCCGAAA
	451				500
1	GCTGAAATCG	AAGGAGATAT	GGGGGATTCC	CACGTCGGTT	TGCAGGCCAG
2	GCTGAAATTG	AAGGTGACAT	GGGTGATTCA	CACGTCGGTT	TACAGGCGCG
3	GCGGAAATTG	AAGGCGACAT	GGGAGATTCC	CATGTCGGTT	TACAAGCACG
4	GCGGAAATTG	AAGGCGACAT	GGGAGATTCC	CATGTCGGTT	TACAAGCACG
	501				550
1	ACTGATGTCT	CAGGCGCTTC	GCAAGCTTTC	CGGAGCGATC	AATAAATCGA
2	TCTCATGTCT	CAGGCGCTCC	GTAAGCTTTC	CGGCGCCATC	AATAAATCTA
3	CTTAATGTCT	CAAGCGCTTC	GTAAGCTTTC	AGGGGCCATT	AACAAATCGA
4	CTTAATGTCT	CAAGCGCTTC	GTAAGCTTTC	AGGGGCCATT	AACAAATCGA
	551				600
1	AGACCATCGC	GATCTTTATC	AACCAGATTC	GTGAAAAAGT	CGGTGTCTATG
2	AAACAATCGC	AATCTTTATT	AACCAGATTC	GTGAAAAAGT	CGGCGTTATG
3	AGACAATCGC	GATTTTCATT	AACCAAATTC	GTGAAAAAGT	CGGTGTTATG
4	AGACAATCGC	GATTTTCATT	AACCAAATTC	GTGAAAAAGT	CGGTGTTATG
	601				650
1	TTTGGAATC	CTGAGACGAC	GCCAGGCGGA	AGAGCGCTGA	AATTCTACTC
2	TTCGGAATC	CGGAGACGAC	ACCGGGCGGC	CGCGCGCTGA	AATTCTATTC
3	TTCGGGAACC	CGGAAACAAC	ACCTGGCGGC	CGTGCGTTGA	AATTCTATTC
4	TTCGGGAACC	CGGAAACAAC	ACCTGGCGGC	CGTGCGTTGA	AATTCTATTC
	651				700
1	TTCTGTCCGC	CTTGAAGTGC	GCCGCGCAGA	GCAGCTGAAA	CAAGGCAACG
2	TTCCGTGCGT	CTTGAAGTGC	GCCGTGCCGA	GCAATTAAAG	CAGGGCAACG
3	TTCCGTGCGT	CTTGAAGTGC	GCCGTGCTGA	ACAGCTGAAA	CAAGGCAACG
4	TTCCGTGCGT	CTTGAAGTGC	GCCGTGCTGA	ACAGCTGAAA	CAAGGCAACG

Figure 2 / Part III

```

701                                     750
1  ACGTCATGGG GAACAAGACG AAAATCAAAG TCGTGAAAAA CAAAGTGGCA
2  ACGTTATGGG GAATAAAACG AGAATTAAAG TCGTAAAAAA CAAAGTCGCT
3  ACGTAATGGG GAACAAAACG AAAATCAAAG TCGTGAAAAA CAAGGTGGCT
4  ACGTAATGGG GAACAAAACG AAAATCAAAG TCGTGAAAAA CAAGGTGGCT

751                                     800
1  CCTCCATTCC GGACAGCCGA AGTGGACATT ATGTACGGGG AAGGAATTTTC
2  CCTCCGTTCC GTACGGCTGA AGTGGACATT ATGTACGGTG AAGGAATCTC
3  CCGCCGTTCC GTACAGCCGA GGTGACATT ATGTACGGAG AAGGCATTTTC
4  CCGCCGTTCC GTACAGCCGA GGTGACATT ATGTACGGAG AAGGCATTTTC

801                                     850
1  AAAAGAAGGG GAAATCATCG ACCTCGGAAC AGAGCTTGAC ATCGTTCAAA
2  CAAAGAAGGG GAAATCATCG ACCTTGGAAC TGAAGTTGAT ATCGTGCAAG
3  AAAAGAAGGC GAAATCATCG ATCTAGGAAC TGAAGTTGAT ATCGTGCAAG
4  AAAAGAAGGC GAAATCATCG ATCTAGGAAC TGAAGTTGAT ATCGTGCAAG

851                                     900
1  AGAGCGGTGC ATGGTACTCT TATCAGGAGG AACGCCTTGG ACAAGGCCGT
2  AAAGCGGCTC GTGGTATTCT TATGAAGAAG AACGCCTCGG ACAGGCCCGT
3  AAAGCGGTTC ATGGTACTCT TATGAAGAAG AGCGTCTTGG CCAAGGCCGT
4  AAAGCGGTTC ATGGTACTCT TATGAAGAAG AGCGTCTTGG CCAAGGCCGT

901                                     950
1  GAAAACGCCA AACAGTTCCT GAAAGAAAAC AAGGATATCC TTTTGATGAT
2  GAAAACGCCA AGCAGTTCCT AAAAGAAAAT AAAGACATCA TGCTGATGAT
3  GAAAATGCAA AACAATTCCT GAAAGAAAAT AAAGATATCA TGCTGATGAT
4  GAAAATGCAA AACAATTCCT GAAAGAAAAT AAAGATATCA TGCTGATGAT

951                                     1000
1  TCAAGAGCAG ATCCGGGAGC ACTACGGTTT GGATACTGGA GGCCTGCTC
2  TCAAGAACAA ATCCGTGAAC ATTACGGTTT GGACAATAAC GGTGTTAC..
3  CCAGGAGCAA ATTCGCGAAC ATTACGGCTT GGATAATAAC GGAGTAGTGC
4  CCAGGAGCAA ATTCGCGAAC ATTACGGCTT GGATAATAAC GGAGTAGTGC

1001                                     1050
1  CTGCACAGGA AGACGAGGCC CAAGCTCAGG AAGAACTCGA GTTTTAATCA
2  .....GGA AAAAGCGGAA GAAGTTCAGG AAGAGCTTGA ATTCGAAGAA
3  .....AGCA GCAAGCTGAA GAGACACAAG AAGAACTCGA ATTTGAAGAA
4  .....AGCA GCAAGCTGAA GAGACACAAG AAGAACTCGA ATTTGAAGAA

1051
1  TGA
2  TAA
3  ...
4  TAA

```

Figure 3

A

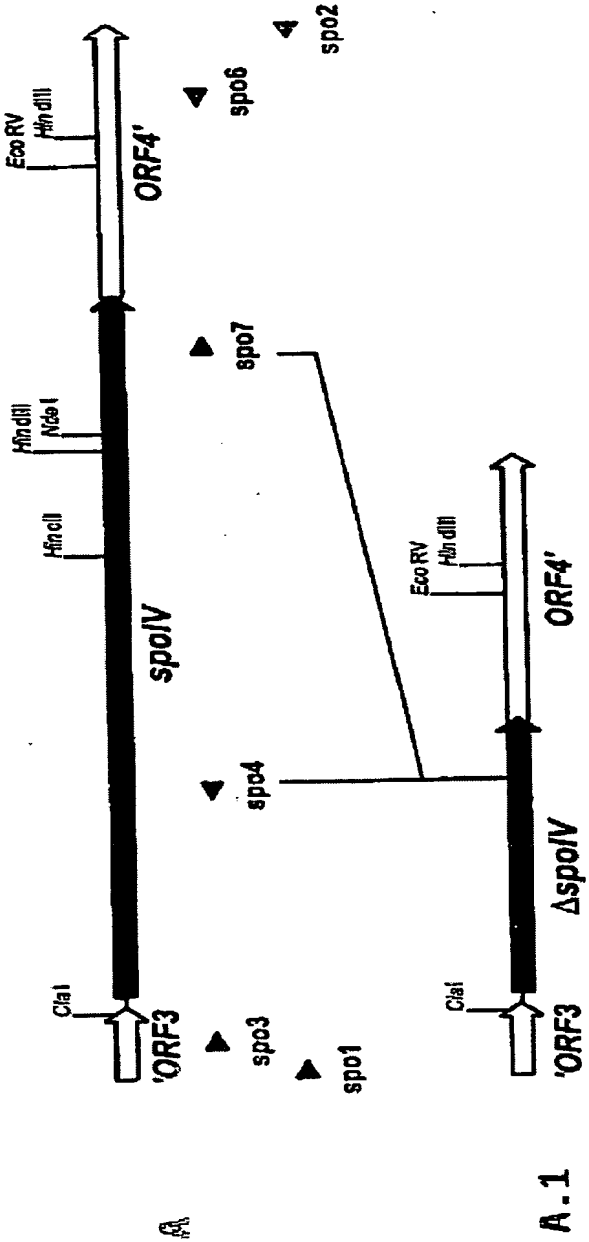


Figure 3

B

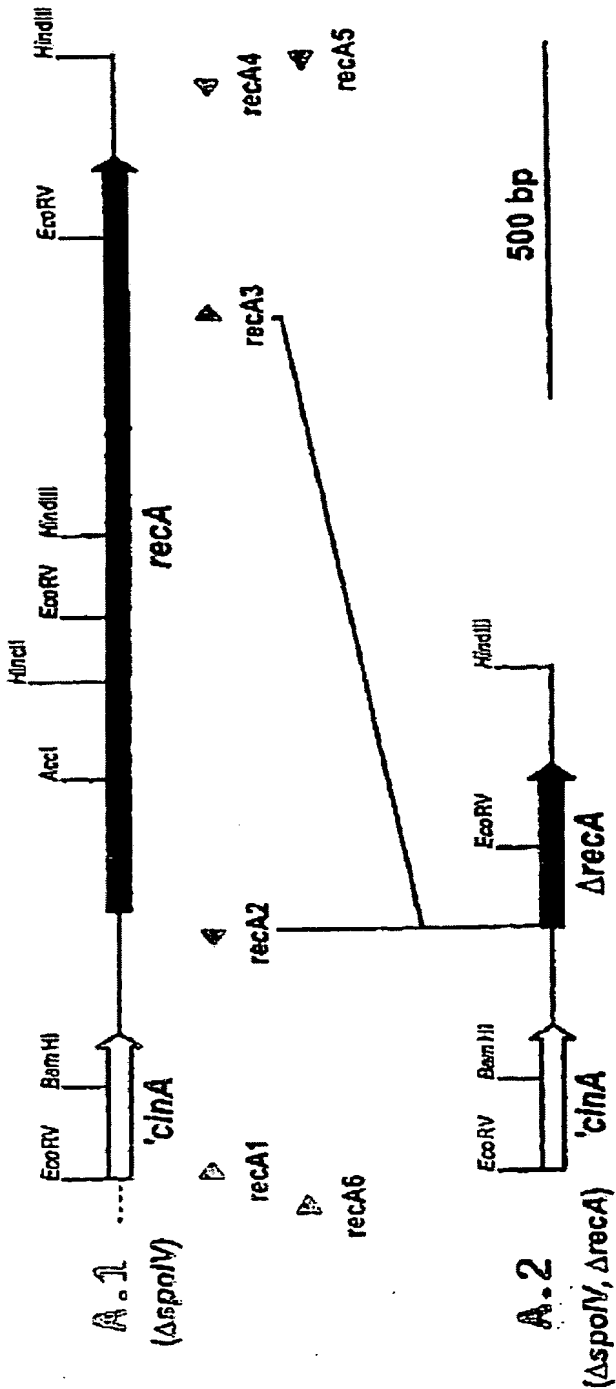


Figure 4

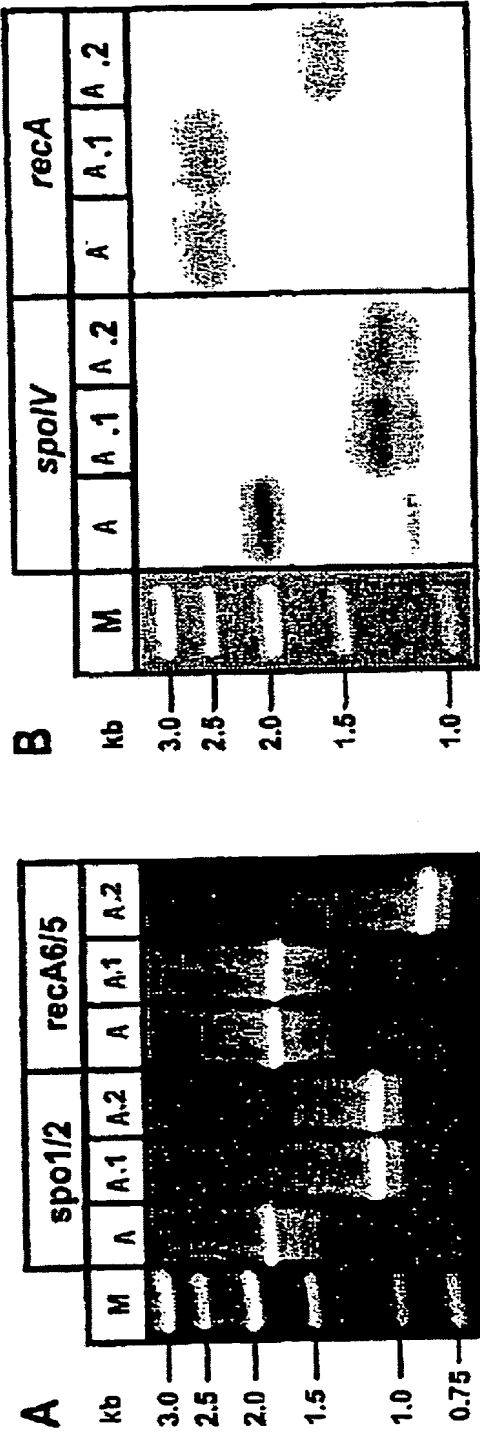


Figure 5

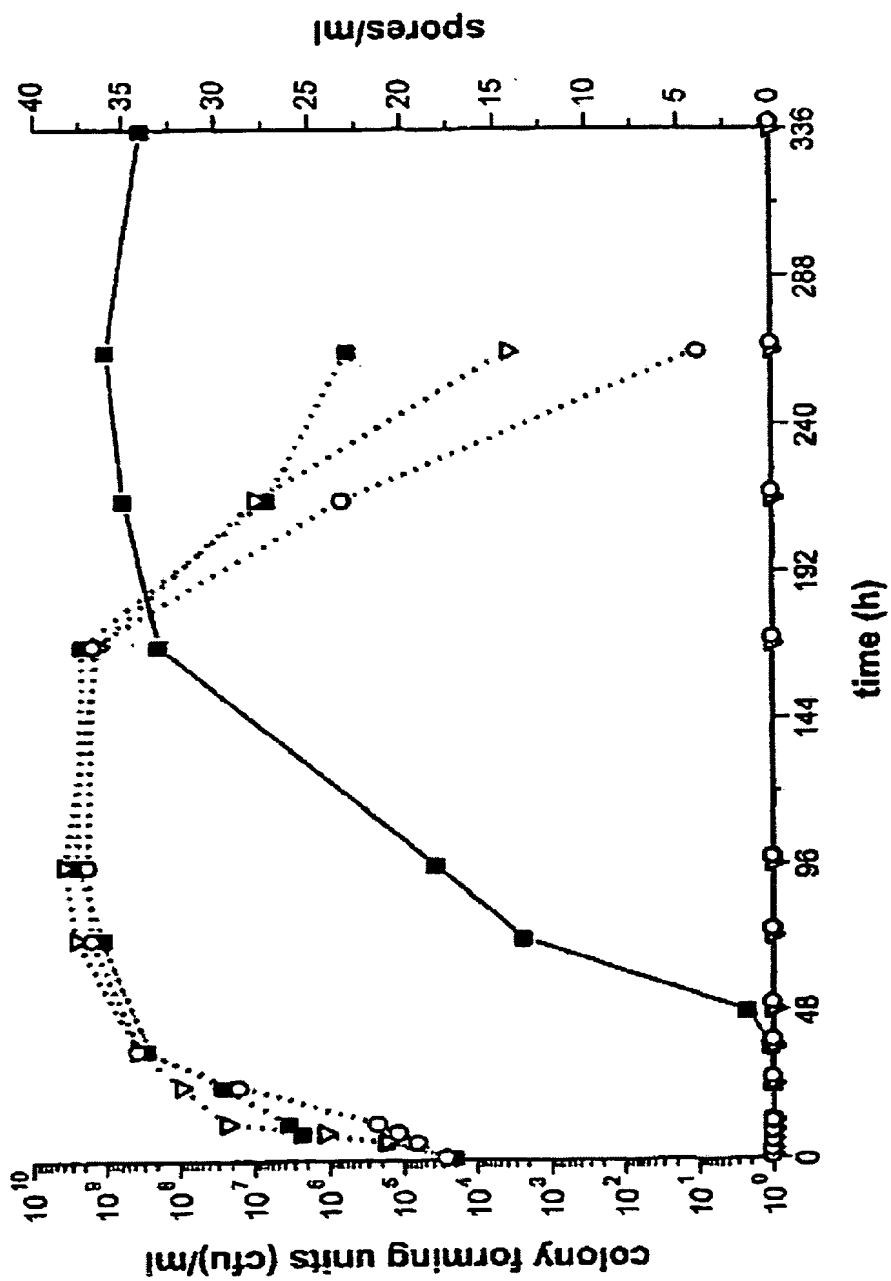


Figure 6

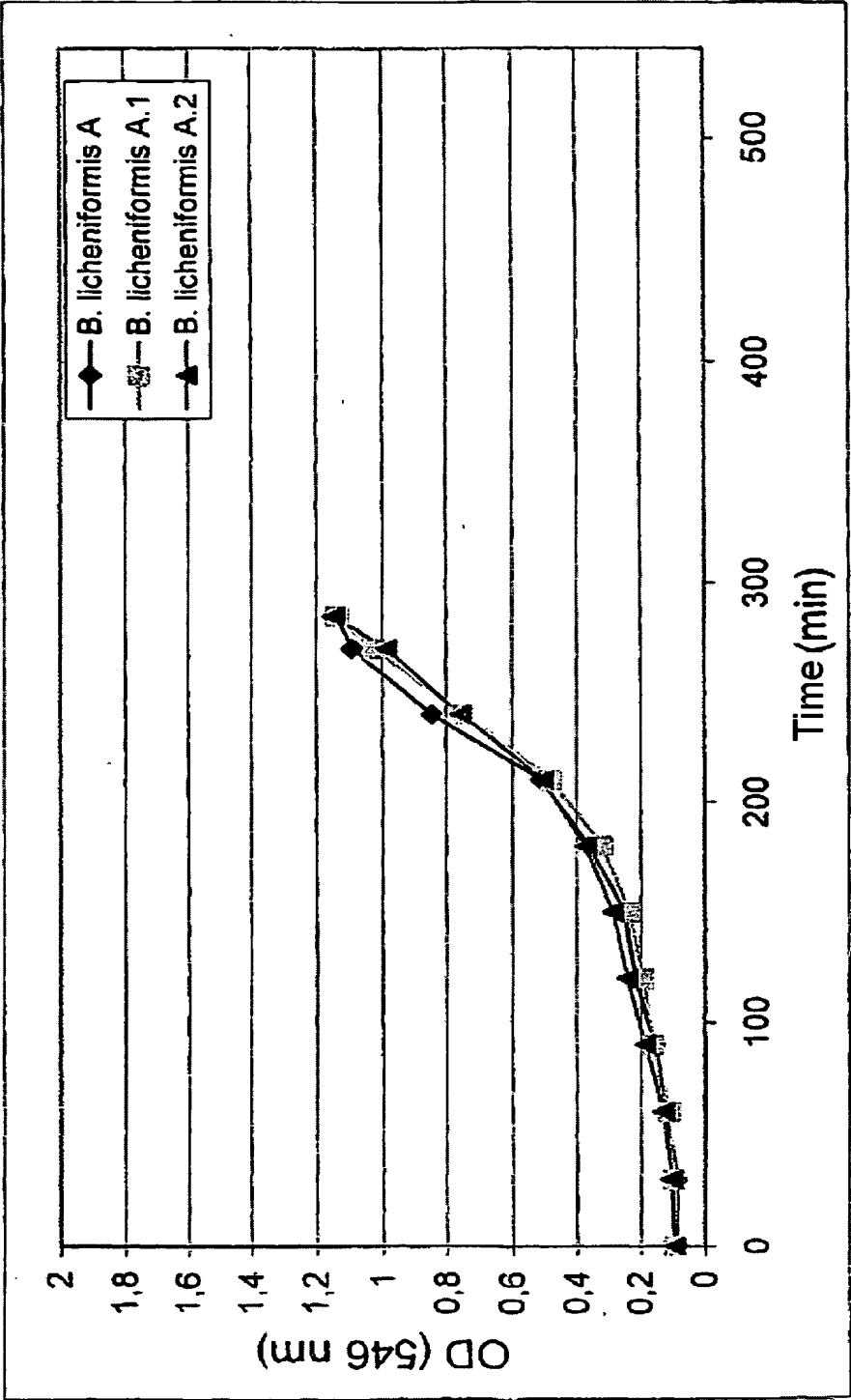
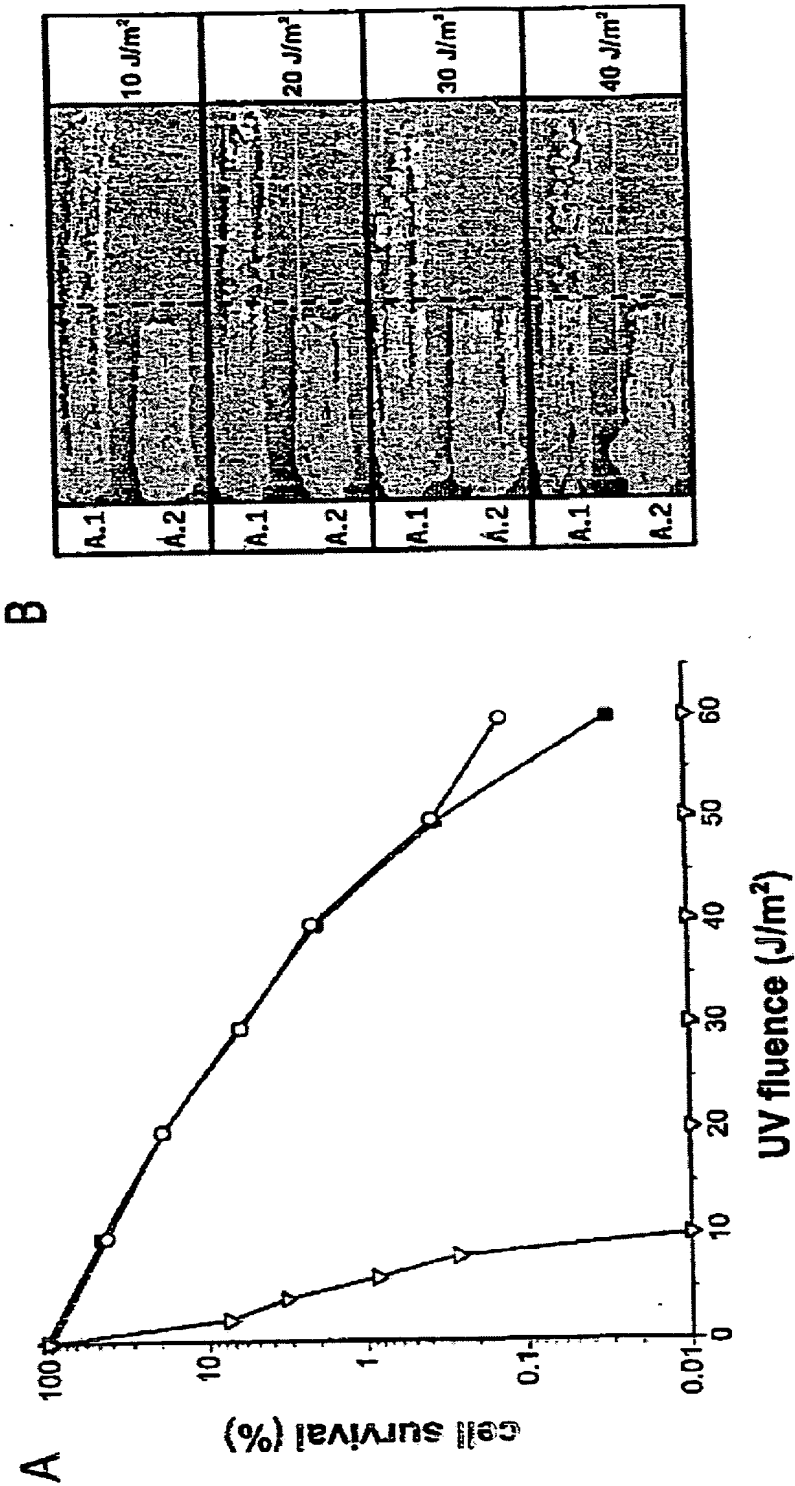


Figure 7



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